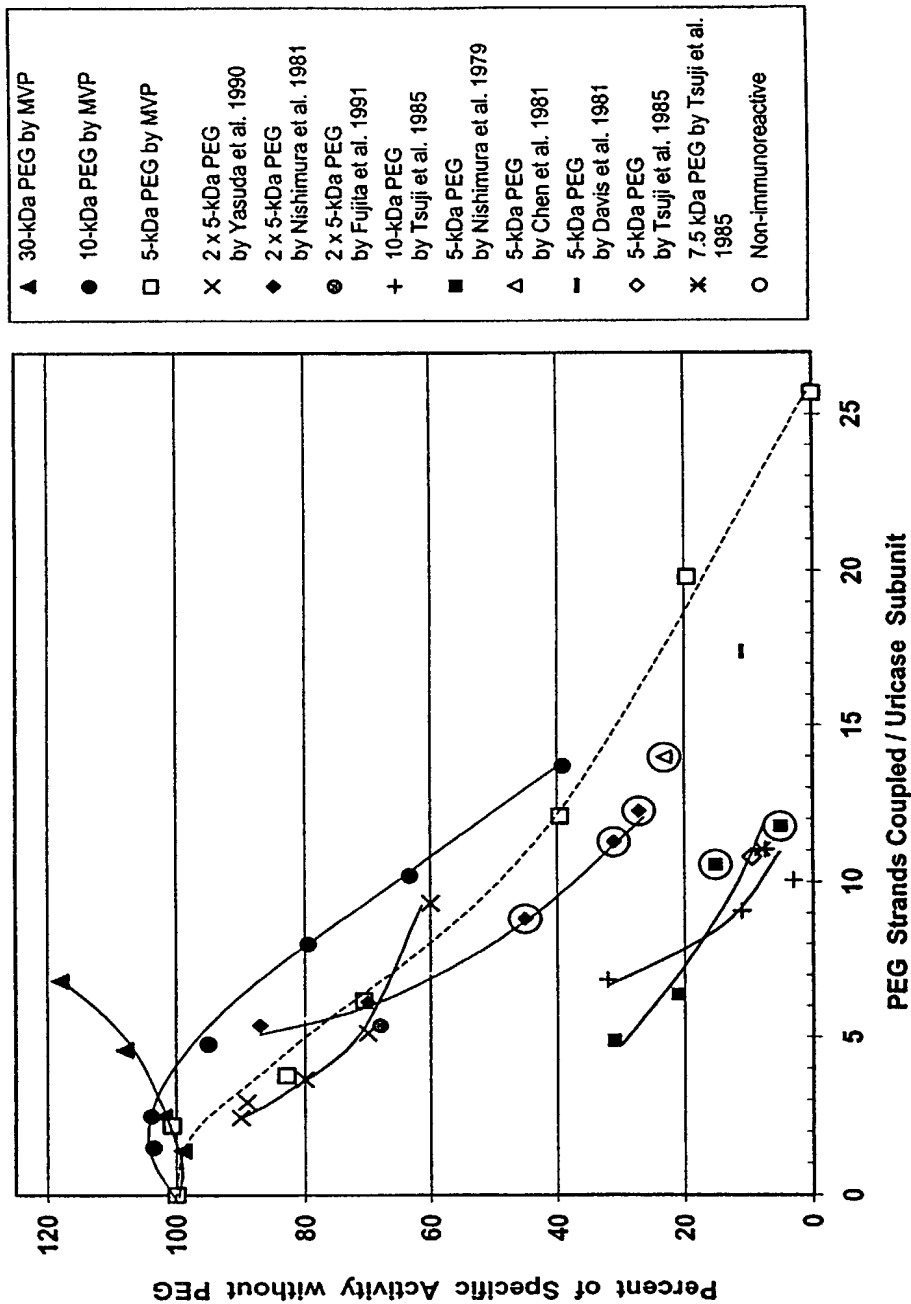
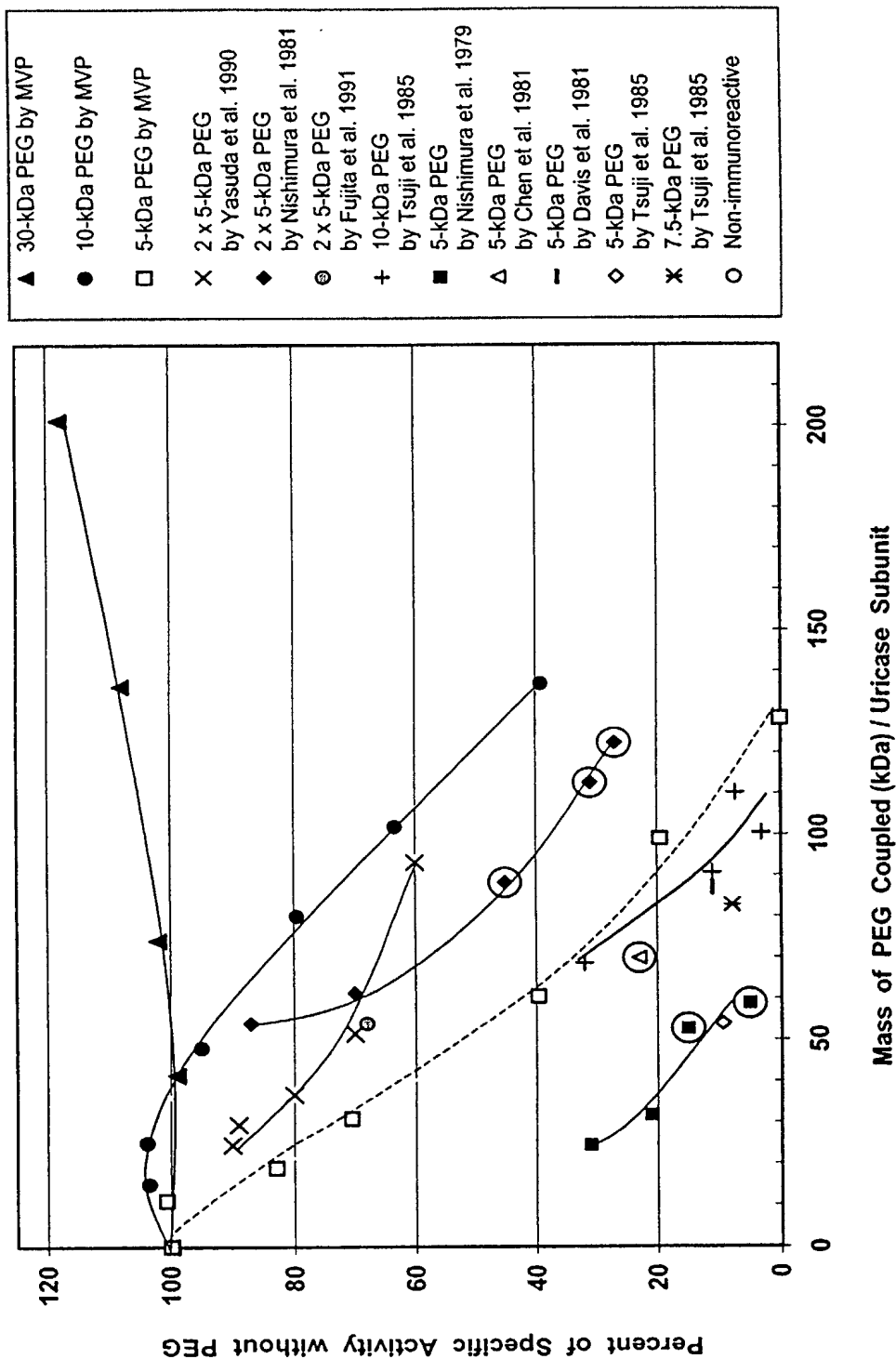


Figure 1A: Retention of Activity by PEGylated Candida Uricase





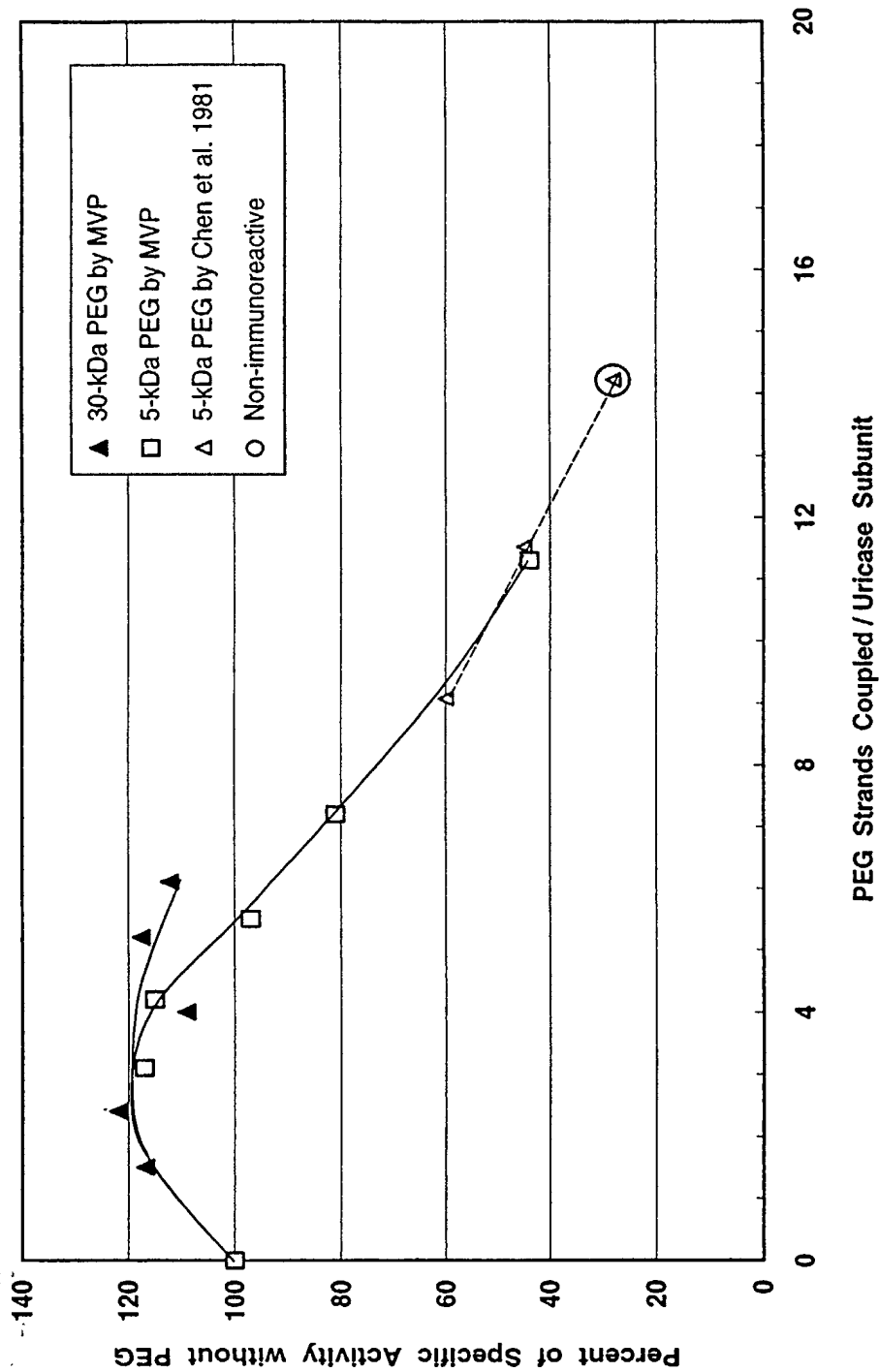
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Figure 2A: Retention of Activity by PEGylated Porcine Uricase



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Figure 2B: Retention of Activity by PEGylated Porcine Uricase

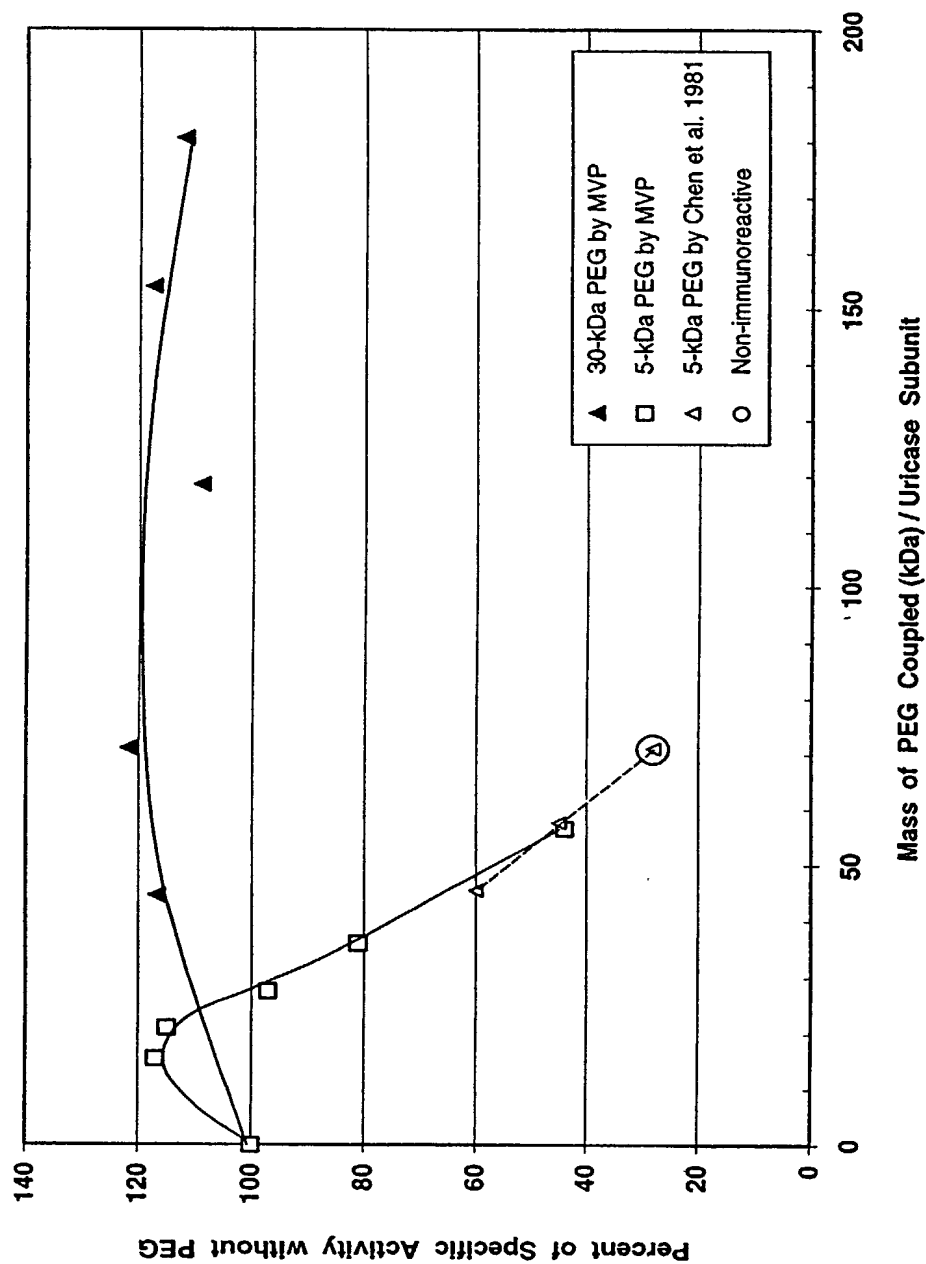
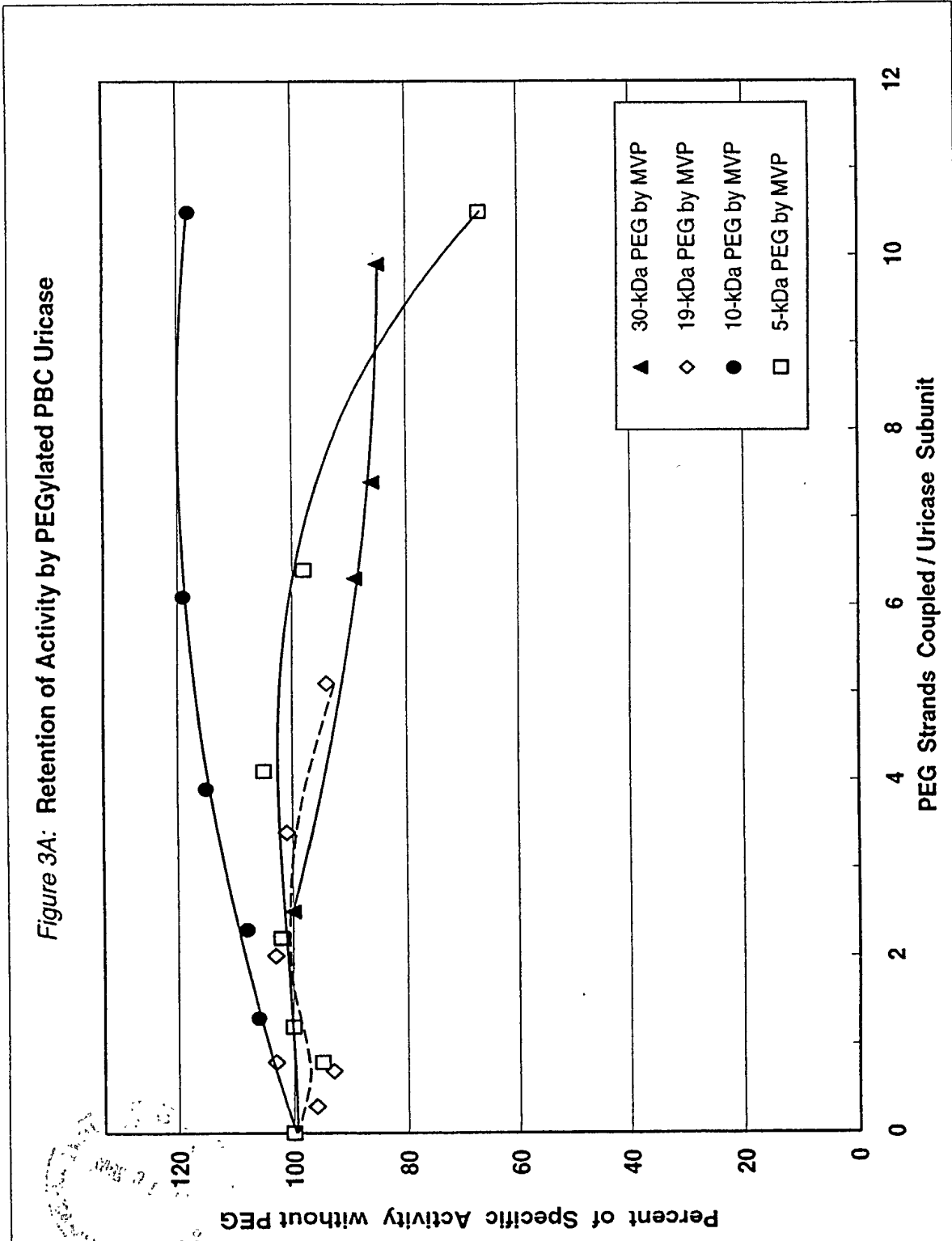


Figure 3A: Retention of Activity by PEGylated PBC Uricase



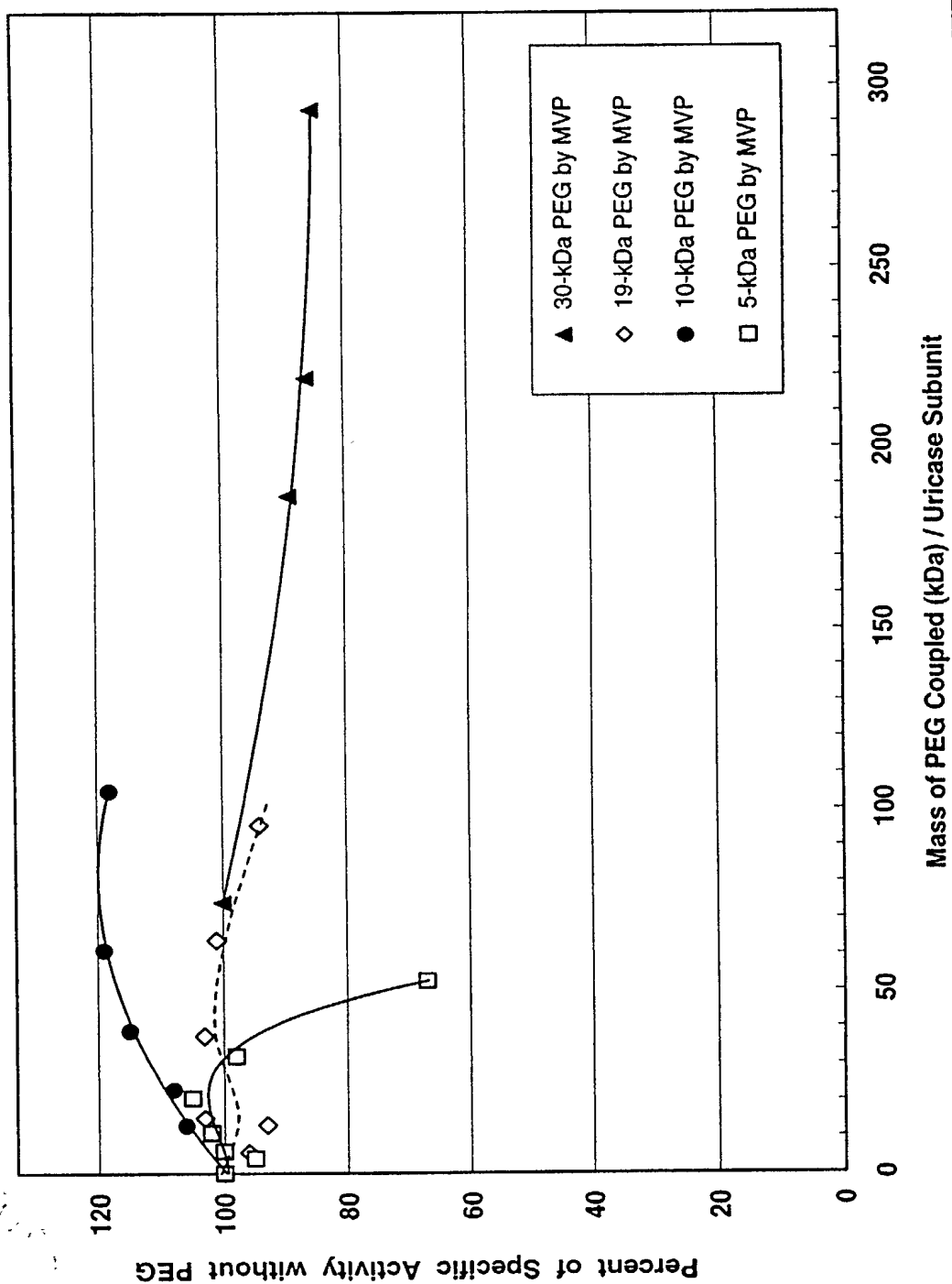
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Figure 3B: Retention of Activity by PEGylated PBC Uricase



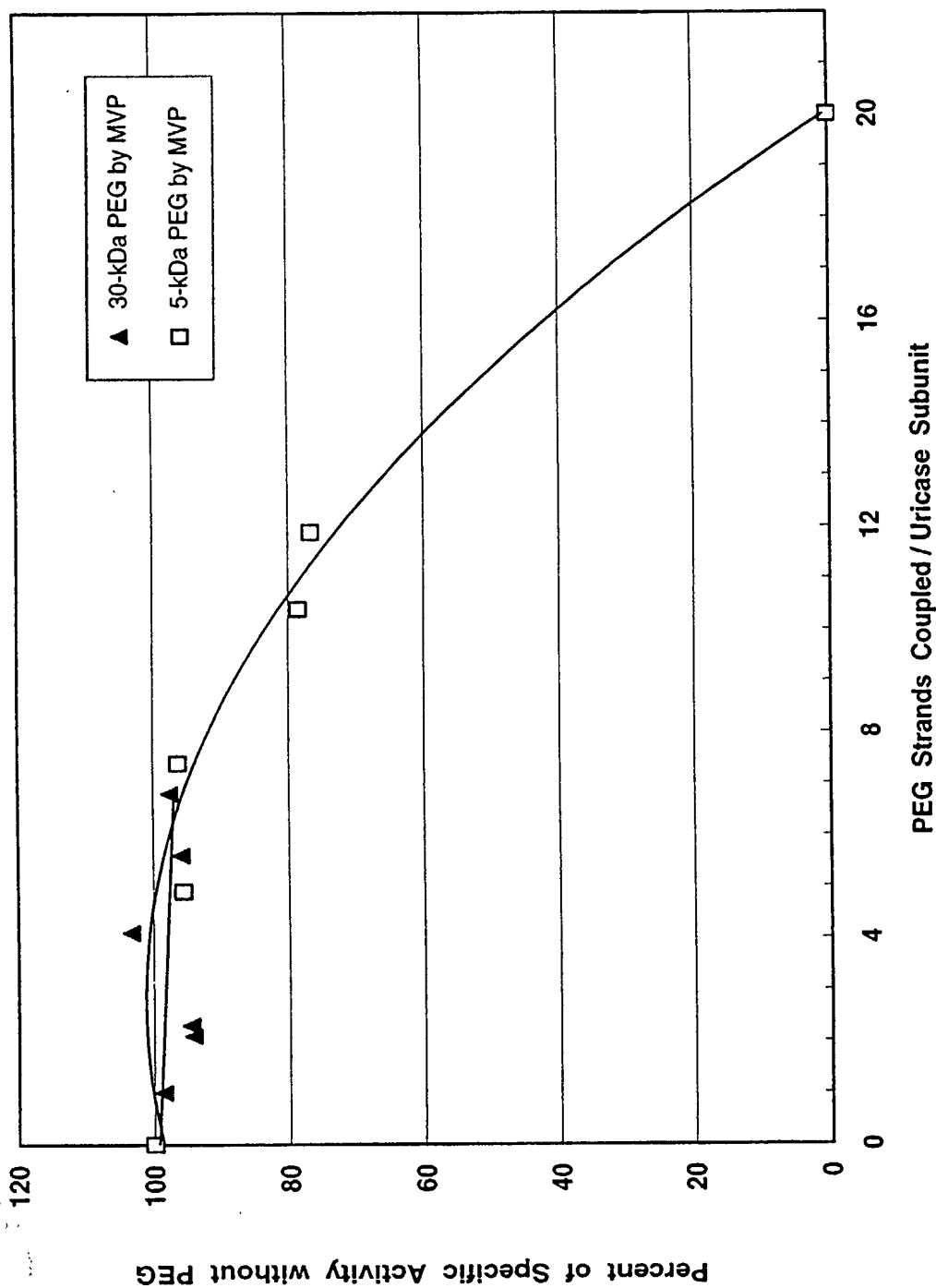
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Figure 4A:
Retention of Activity by PEGylated Uricozyme® (*A. flavus* Uricase)



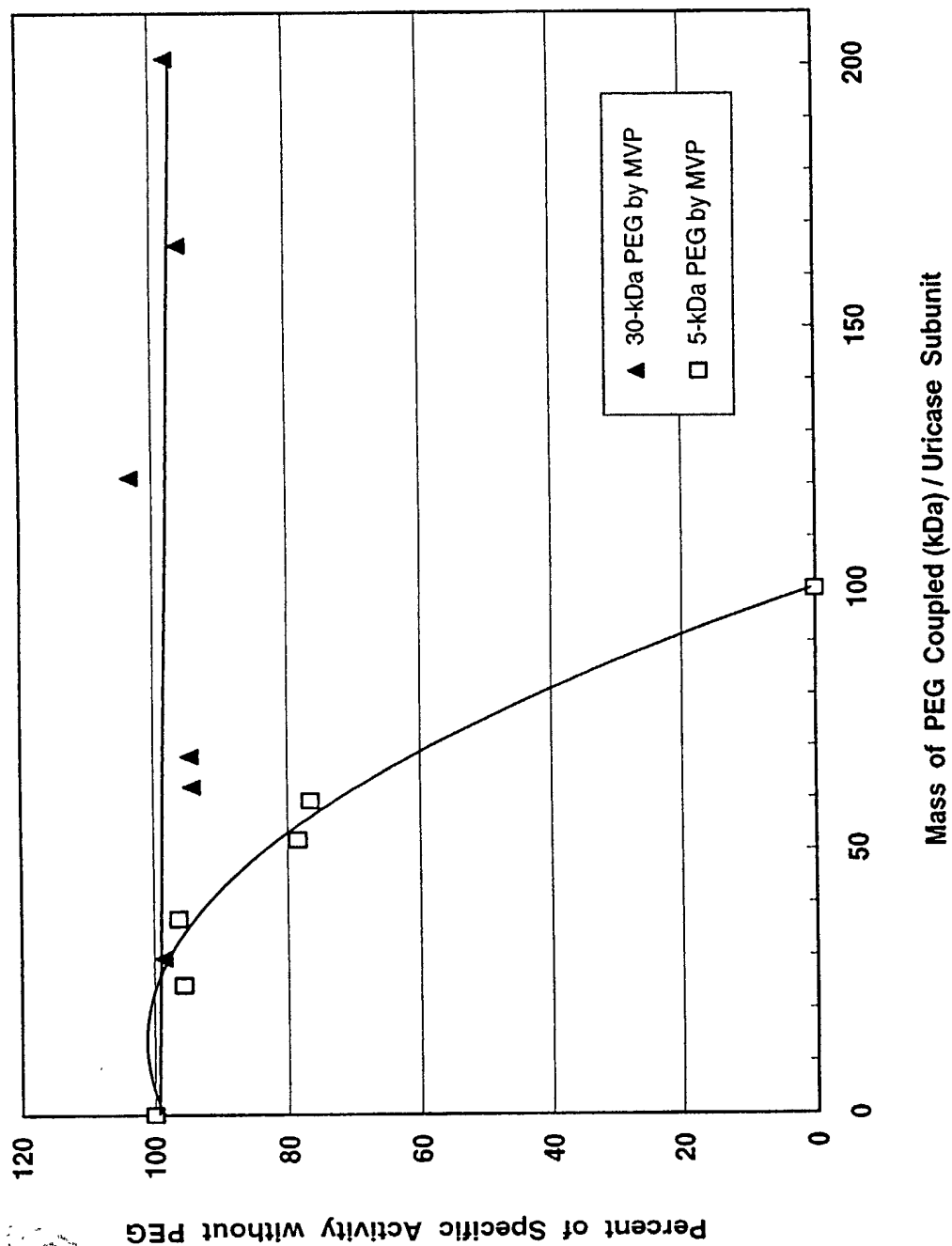
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Figure 4B:
Retention of Activity by PEGylated Uricozyme® (*A. flavus* Uricase)



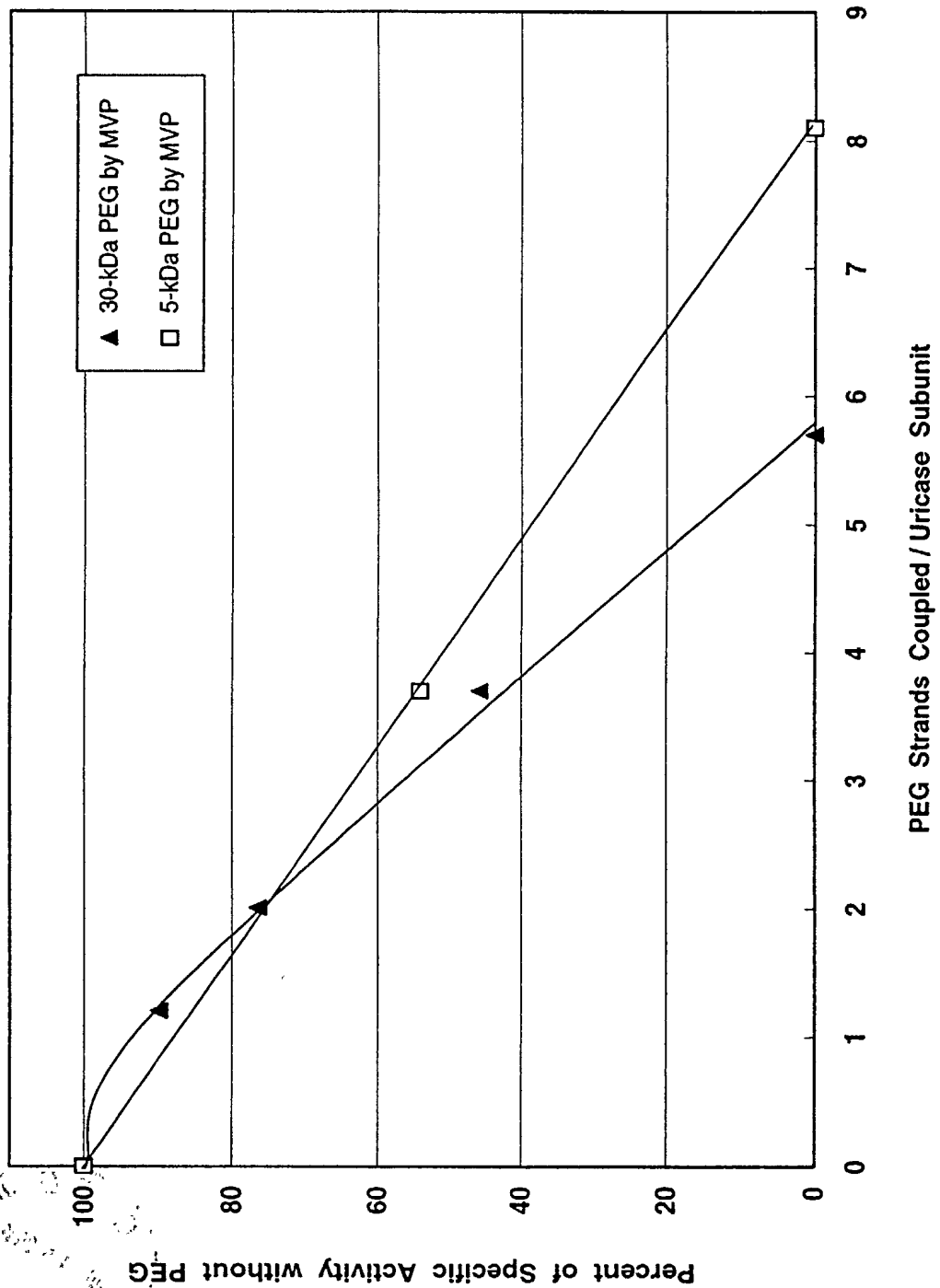
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Figure 5A: Retention of Activity by PEGylated Soybean Uricase



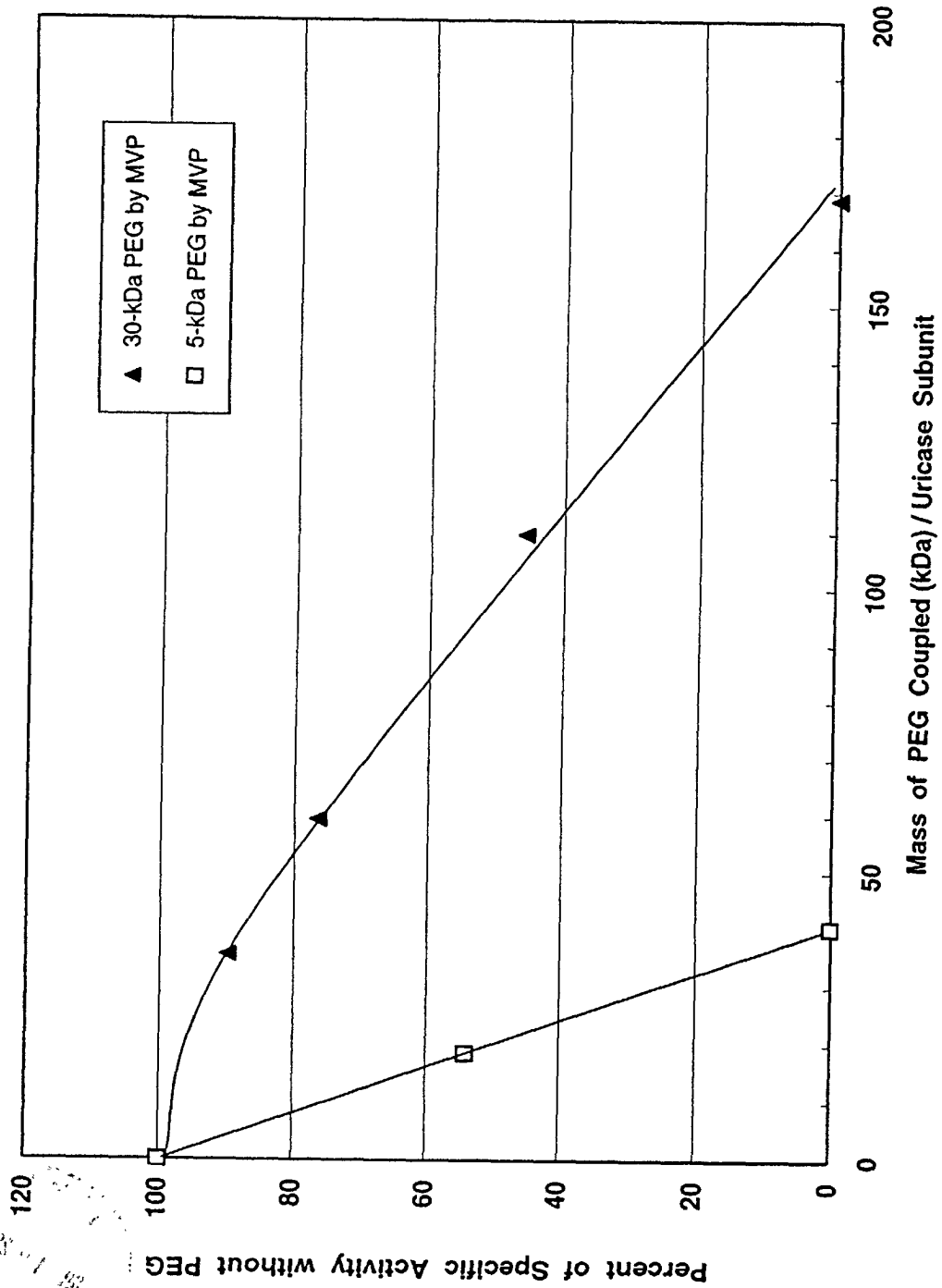
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Figure 5B: Retention of Activity by PEGylated Soybean Uricase



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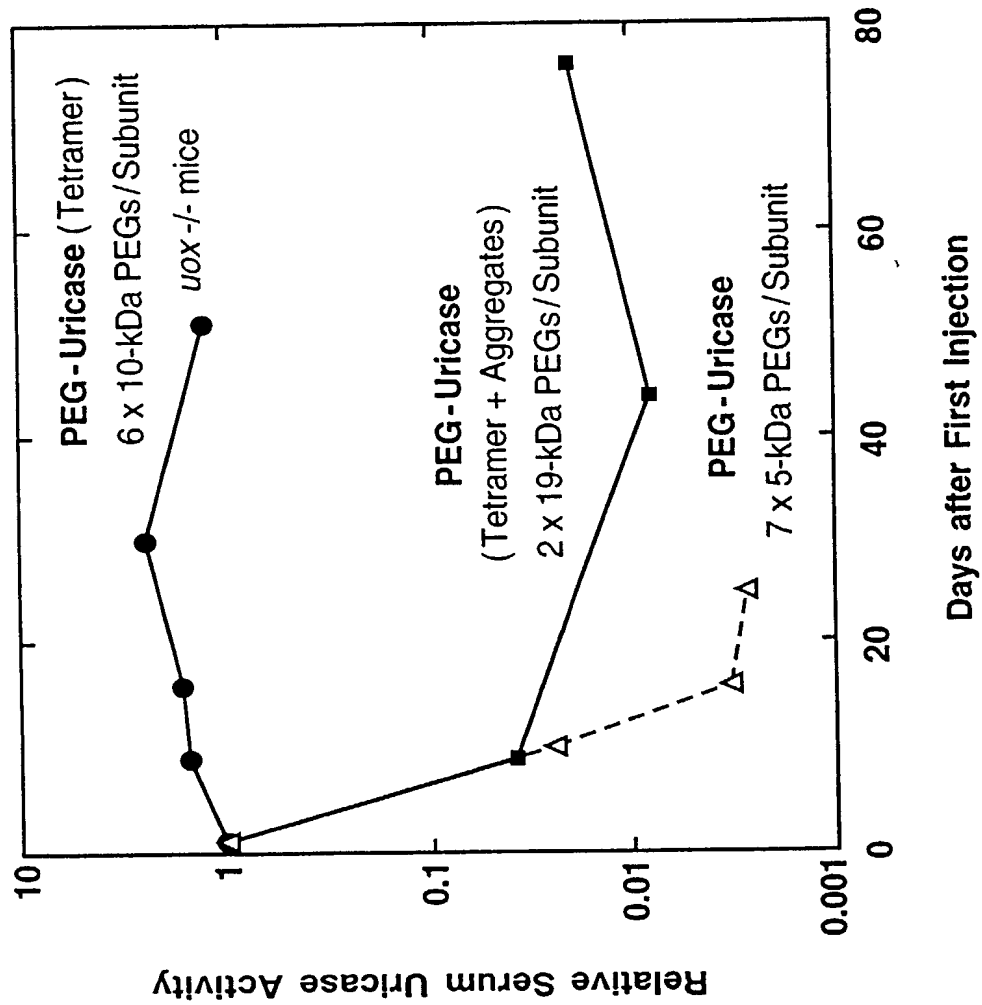
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Figure 6: Deduced amino acid sequences of Pig-Baboon Chimeric (PBC) uricase, PBC uricase that is truncated at the amino and carboxyl terminals (PBC-NT-CT) and Porcine uricase containing the mutations R291K and T301S (PKS Uricase) (SEQ ID NO:3), compared with the porcine sequence (SEQ ID NO: 1) and baboon sequence (SEQ ID NO: 2)

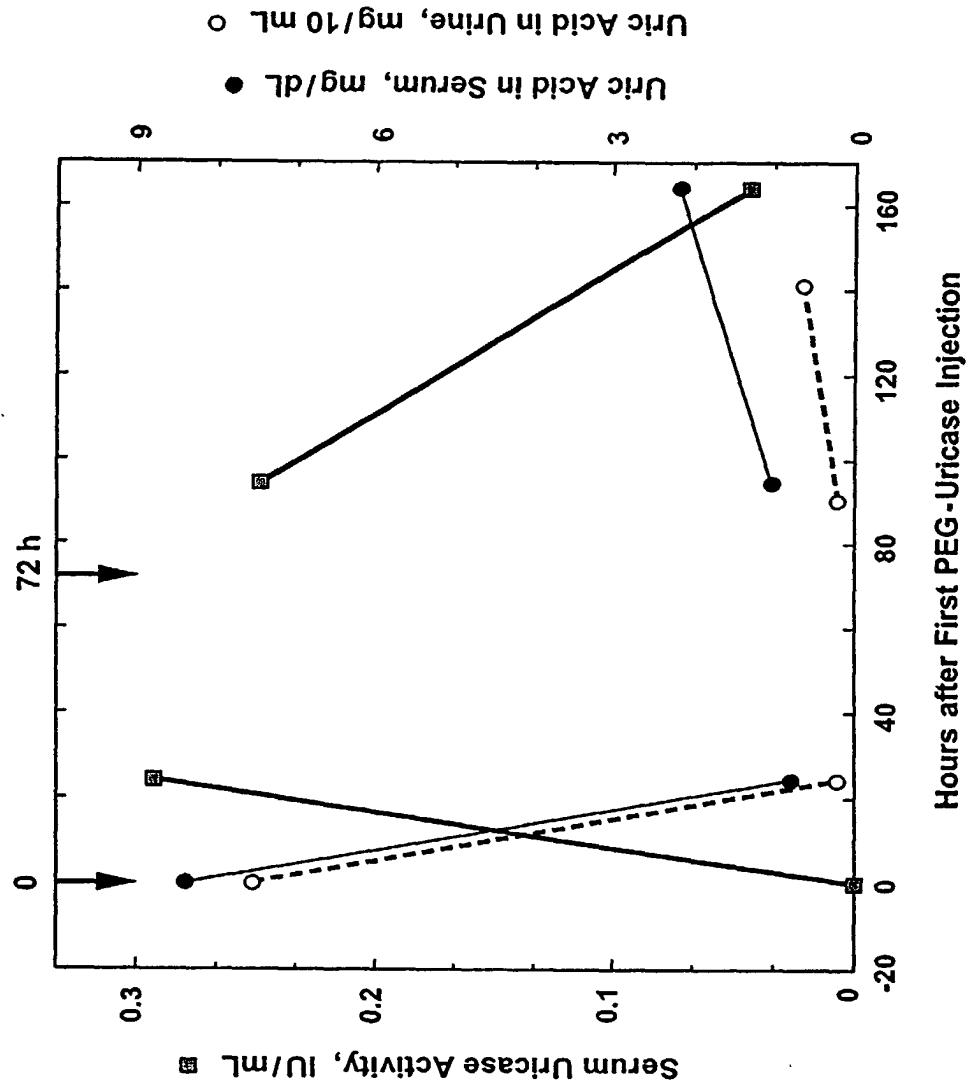
Porcine	MAHYRNDYKK NDEVEFVRTG YGKDMIKVLH IQRDGKYHSI	40
PBC	porcine sequence 1-225 →	40
PBC-NT-CT	porcine sequence 1-219 →	34
PKS	porcine sequence 1-288 →	40
Baboon	MADYHNNYKK NDELEFVRTG YGKDMVKVLH IQRDGKYHSI	40
Porcine	KEVATSVQLT LSSKKDYLHG DNSDVIPTDT IKNTVNVLAK	80
PBC	porcine sequence →	80
PBC-NT-CT	porcine sequence →	74
PKS	porcine sequence →	80
Baboon	KEVATSVQLT LSSKKDYLHG DNSDIPTDT IKNTVHVLAK	80
Porcine	FKGIKSIETF AVTICEHFLS SFKHVIRAQV YVEEVPWKRF	120
PBC	porcine sequence →	120
PBC-NT-CT	porcine sequence →	114
PKS	porcine sequence →	120
Baboon	FKGIKSIEAF GVNICEYFLS SFNHVIRAQV YVEEIPWKRL	120
Porcine	EKNGVKHVHA FIYTPTGTHF CEVEQIRNGP PVIHSGIKDL	160
PBC	porcine sequence →	160
PBC-NT-CT	porcine sequence →	154
PKS	porcine sequence →	160
Baboon	EKNGVKHVHA FIHTPTGTHF CEVEQLRSGP PVIHSGIKDL	160
Porcine	KVLKTTQSGF EGFIKDQFTT LPEVKDRCFA TQVYCKWRYH	200
PBC	porcine sequence →	200
PBC-NT-CT	porcine sequence →	194
PKS	porcine sequence →	200
Baboon	KVLKTTQSGF EGFIKDQFTT LPEVKDRCFA TQVYCKWRYH	200
Porcine	QGRDVFDEAT WDTVRSIVLQ KFAGPYDKGE YSPSVQKTLY	240
PBC	porcine sequence → ← baboon sequence	240
PBC-NT-CT	porcine sequence → ← baboon sequence	234
PKS	porcine sequence →	240
Baboon	QCRDVFDEAT WGTIRDLVLE KFAGPYDKGE YSPSVQKTLY	240
Porcine	DIQVLTGQV PEIEDMEISL PNIHYLNIDM SKMGLINKEE	280
PBC	baboon sequence →	280
PBC-NT-CT	baboon sequence →	274
PKS	porcine sequence →	280
Baboon	DIQVLSLSRV PEIEDMEISL PNIHYFNIDM SKMGLINKEE	280
Porcine	VLLPLDNPYG RITGTVKRKL TSRL	304
PBC	baboon sequence →	304
PBC-NT-CT	baboon sequence →	295
PKS	porcine ← baboon →	304
Baboon	VLLPLDNPYG KITGTVKRKL SSRL	304

Figure 7: Serum Uricase Activity 24 Hours after Each PEG-Uricase Injection, Relative to the First Injection



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Figure 8: Inverse Relationship between Serum PEG-Uricase Activity and Uric Acid Levels in the Serum and Urine of a Uricase-Deficient Mouse



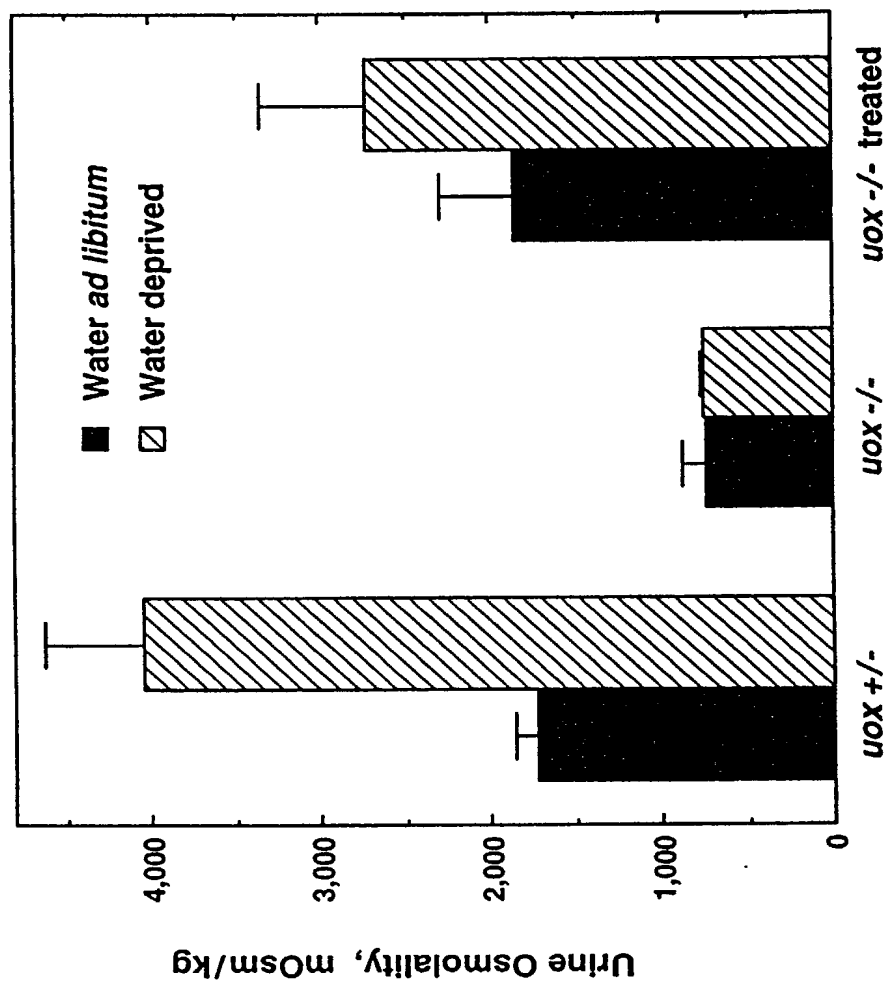
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Figure 9: Decreased Severity of Urine-Concentrating Defect
in Uricase-Deficient Mice Treated with PEG-Uricase



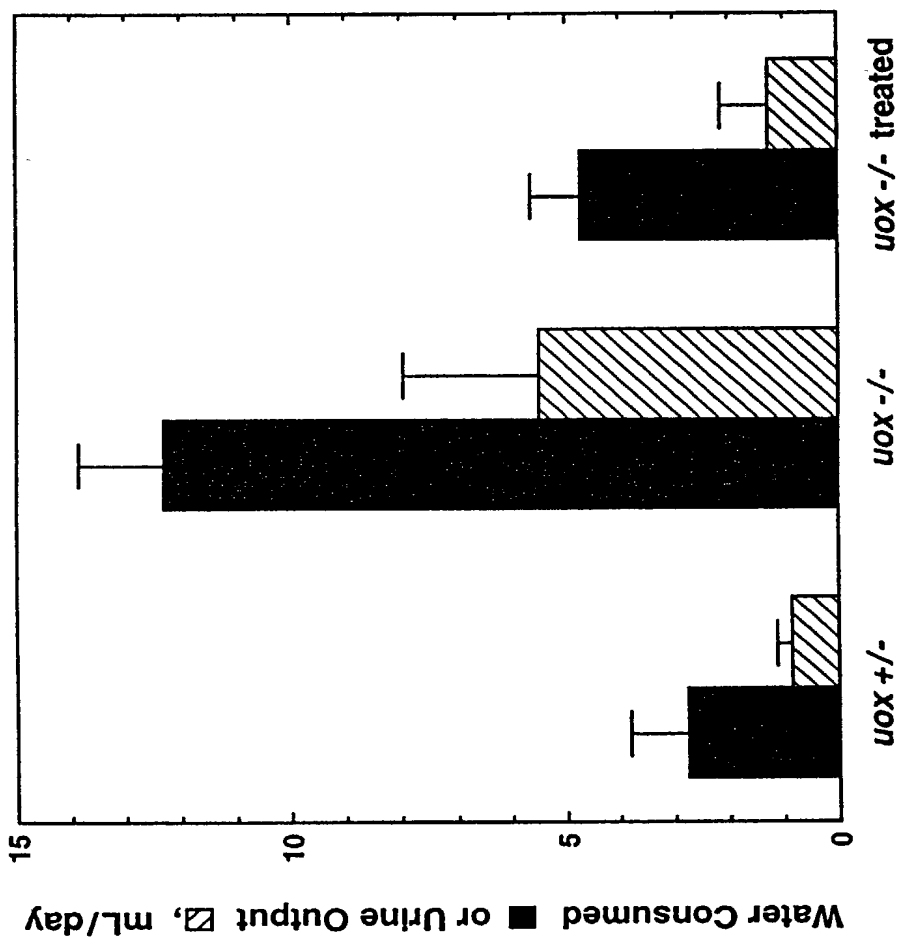
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Figure 10: Decreased Severity of Nephrogenic Diabetes Insipidus
in Uricase-Deficient Mice Treated with PEG-Uricase



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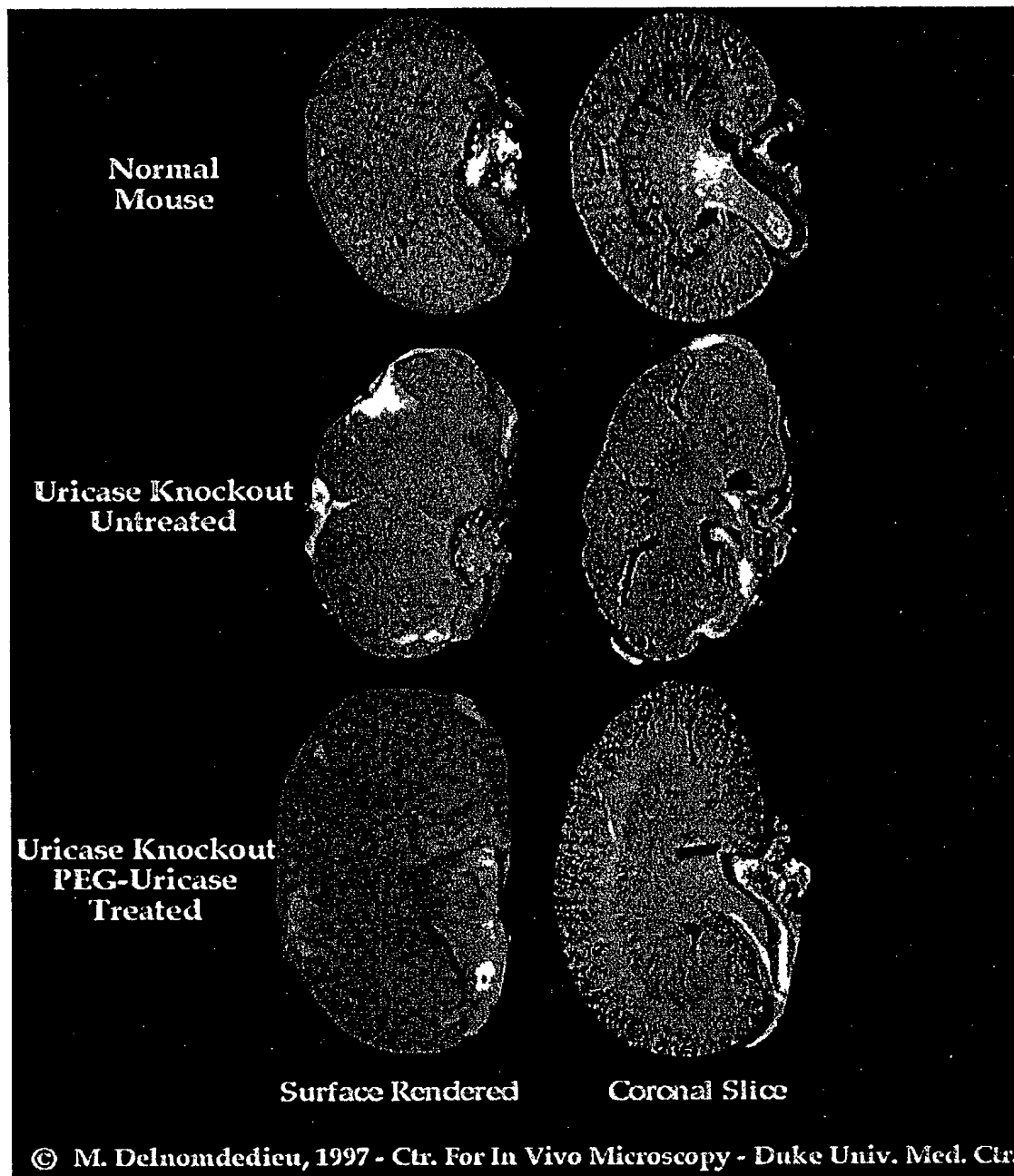
Figure 11:**Decreased Severity of Uric Acid-Induced Nephropathy after Treatment with PEG-Uricase, as Visualized by Magnetic Resonance Microscopy**

Figure 12: Clearance from the Circulation of BALB/c Mice of PBC Uricase Tetramer and Octamer Coupled to 5-6 Strands of 10-kDa PEG/Subunit

